RESPONSE

I. Status of the Claims

Claim 6 has been cancelled without prejudice or disclaimer as being drawn to a non-elected invention. Claim 7 has been amended. Claims 2-5 and 7-11 are therefore presently pending in the case. In an attempt to comply with the revised 37 C.F.R. §1.121 and for the convenience of the Examiner the status of the claims is described hereto as **Exhibit A.**

II. Support for the Amended Specification and Claims

Claim 7 has been amended in response to an objection and to further clarify the claim. Amendment of Claim 7 finds support throughout the specification as originally filed with particular support being provided by the original Claim 1 and the Sequence Listing as originally filed.

As the amendments of Claim 7 is fully supported by the specification and claims as originally filed, they do not constitute new matter. Entry therefore is respectfully requested.

III. Rejection of Claims 2-5 and 7-11 Under 35 U.S.C. § 101

The Action first rejects claims 2-5 and 7-11 under 35 U.S.C. § 101 because the claimed invention lacks patentable utility allegedly because the claimed invention is not supported by either a specific and substantial utility or a well established utility.

The Action recognizes that specification describes metalloproteinases (especially zinc metalloproteases of the ADAMTS family) indicates that the sequences of the present invention encode a metalloprotease (in particular ADAMSTS14).

In support of this recognized assertion, Applicants respectfully submit that SEQ ID NO:20 of the present invention is nearly identical to a sequence that is present in the leading scientific repository for biological sequence data (GENBANK). This sequence, GENBANK Accession No. Q8WXS8(information provided as **Exhibit B**) has been annotated by third party scientists *wholly unaffiliated with Applicants* as "ADAMTS-14 precursor (A disintegrin and metalloproteinase with thrombospondin motifs 14) (ADAM-TS 14)". Thus Applicants' assertion that the sequences of the

present invention represent a variant of Q8WXS8 is supported by the evidence provided in **Exhibit C**, which contains an amino acid sequence comparison between SEQ ID NO:20 and the amino acid sequence of Q8WXS8. From this comparison, it can be seen that SEQ ID NO:20 shares a greater than 95% homology with the amino acid sequence of Q8WXS8.

Tissues which express the sequences of the present invention were described in the specification (page 3, line 5) as being human spinal cord, lymph node, bone marrow, trachea, mammary gland, skeletal muscle, pericardium, adipose, esophagus, bladder, fetal kidney, and fetal lung cells. The activity of the protein encoded by the sequences of the present invention is described in several publications (Abstracts provided as **Exhibit D**). One is entitled "Characterization of ADAMTS14, a novel member of the ADAMTS metalloproteinase family" by Bolz *et al.*, 2001 (Biochim Biophys Acta. *1522*:221-5, 2001). A second is entitled "Cloning and characterization of ADAMTS-14, a novel ADAMTS displaying high homology with ADAMTS-2 and ADAMTS-3" by Colige, *et al.*, 2002 (J Biol Chem. *277*:5756-66, 2002, Epub 2001 Dec 07). The third is entitled "Cloning, expression analysis, and structural characterization of seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains" by Cal, *et al.*, 2002 (Gene *283*:49-62).

Applicants respectfully submit that these publications constitutes evidence that clearly demonstrates that the proteins of the present invention have function and utility that are both accepted by those skilled in the art. As the legal test for utility simply involves an assessment of whether those skilled in the art would find any of the utilities described for the invention to be credible or believable. Clearly those of skill in the art would recognize that molecules that share such amino acid sequence homology would share protein structure and would thus would also share the same function. This constitutes evidence that clearly supports the specifications assertion that SEQ ID NO:19 and 20 encode a known protein (the metalloprotease ADAMSTS14).

Applicants submit that the presently claimed molecules have been shown to encode, as asserted in the specification as filed, ADAMTS-14 precursor (A disintegrin and metalloproteinase with thrombospondin motifs 14) (ADAM-TS 14) which is known to the art. Thus, the present situation directly tracks Example 10 of the Revised Interim Utility Guidelines Training Materials (pages 53-55), which establishes that a rejection under 35 U.S.C. § 101 as allegedly lacking a patentable utility and

under 35 U.S.C. § 112, first paragraph as allegedly unusable by the skilled artisan due to the alleged lack of patentable utility, is not proper when a full length sequence (such as the presently claimed sequence), and has a similarity score greater than 95% to a protein having a known function (such as the 100% identity between the presently claimed sequences and those of the cited protein (Q8WXS8).

Further evidence of utility of the presently claimed polynucleotide, although only one is needed to meet the requirements of 35 U.S.C. § 101 (*Raytheon v. Roper*, 220 USPQ 592 (Fed. Cir. 1983); *In re Gottlieb*, 140 USPQ 665 (CCPA 1964); *In re Malachowski*, 189 USPQ 432 (CCPA 1976); *Hoffman v. Klaus*, 9 USPQ2d 1657 (Bd. Pat. App. & Inter. 1988)), is the specific utility the present nucleotide sequence has in determining the genomic structure of the corresponding human chromosome, for example mapping the protein encoding regions as described in the specification. As evidence supporting Applicants assertions of the specific utility of the sequences of the present invention in localizing the specific region of the human chromosome and identification of functionally active intron/exon splice junctions is the information provided as **Exhibit E**. This is the result of overlaying the sequence of SEQ ID NO:**19** of the present invention and the identified human genomic sequence. By doing this, one is able to identify the portions of the genome that encode the present invention. If these regions of the genome are non-contiguous, this is indicative of individual exons. The results of such an analysis indicates that the sequence of the present invention is encoded by at least 24 exons spread non-contiguously along a region of human chromosome 10, which are contained within four BAC clones AL335344.20, AC007484.2, AC069538.10 and AC007484.2. Thus clearly one would not simply be able to identify the 24 or more protein encoding exons that make up the sequence of the present intention from within the large genomic sequence. Nor, would one be able to map the protein encoding regions identified specifically by the sequences of the present invention without knowing exactly what those specific sequences were. Additionally, it should be noted that the human ADAMSTS14 gene also maps to the same region of human chromosome 10 (at approximately 10q2). This further supports Applicant's position that the sequences of the present invention encodes a variant of the human ADAMSTS14.

Therefore, clearly, the present polynucleotide provides exquisite specificity in localizing the specific region of the human chromosome containing the gene encoding the given polynucleotide, a utility not shared by virtually any other nucleic acid sequence. In fact, it is this specificity that makes this

particular sequence so useful. Early gene mapping techniques relied on methods such as Giemsa staining to identify regions of chromosomes. However, such techniques produced genetic maps with a resolution of only 5 to 10 megabases, far too low to be of much help in identifying specific genes involved in disease. The skilled artisan readily appreciates the significant benefit afforded by markers that map a specific locus of the human genome, such as the present nucleic acid sequence.

Only a minor percentage of the genome actually encodes exons, which in turn encode amino acid sequences. The presently claimed polynucleotide sequence provides biologically validated empirical data (*e.g.,* showing which sequences are transcribed, spliced, and polyadenylated) that *specifically* defines that portion of the corresponding genomic locus that actually encodes exon sequence. Equally significant is that the claimed polynucleotide sequence defines how the encoded exons are actually spliced together to produce an active transcript (*i.e.*, the described sequences are useful for functionally defining exon splice-junctions). The Applicants respectfully submit that the practical scientific value of expressed, spliced, and polyadenylated mRNA sequences is readily apparent to those skilled in the relevant biological and biochemical arts. The presently claimed polynucleotide sequence defines a biologically validated sequence that provides a unique and specific resource for mapping the genome.

An additional utility includes the use of the presently claimed polynucleotides on DNA chips. Further, the Action seems to be requiring Applicants to identify the biological role of the nucleic acid or function of the protein encoded by the presently claimed polynucleotides before the present sequences can be used in gene chip applications that meet the requirements of § 101. Applicants respectfully point out that knowledge of the exact function or role of the presently claimed sequence <u>is not required</u> to track expression patterns using a DNA chip. Given the widespread utility of such "gene chip" methods using *public domain* gene sequence information, there can be little doubt that the use of the presently described *novel* sequences would have great utility in such DNA chip applications. The claimed sequence provides a <u>specific</u> marker of the human genome (see evidence below), and that such <u>specific</u> markers are targets for discovering drugs that are associated with human disease. Thus, those skilled in the art would instantly recognize that the present nucleotide sequence would be an ideal, novel candidate for assessing gene expression using, for example, DNA chips, as the specification details. Such "DNA chips" clearly have utility, as evidenced by hundreds of issued U.S. Patents, as

exemplified by U.S. Patent Nos. 5,445,934, 5,556,752, 5,744,305, as well as more recently issued U.S. Patent Nos. 5,837,832, 6,156,501 and 6,261,776. Accordingly, the present sequence has a specific utility in such DNA chip applications. Clearly, compositions that enhance the utility of such DNA chips, such as the presently claimed nucleotide sequence, must also be useful.

Additionally, since only a small percentage of the genome (2-4%) actually encodes exons, which in-turn encode amino acid sequences. Thus, not all human genomic DNA sequences are useful in such gene chip applications. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101. It has been clearly established that a statement of utility in a specification must be accepted absent reasons why one skilled in the art would have reason to doubt the objective truth of such statement. *In re Langer*, 503 F.2d 1380, 1391, 183 USPQ 288, 297 (CCPA, 1974); *In re Marzocchi*, 439 F.2d 220, 224, 169 USPQ 367, 370 (CCPA, 1971).

Evidence of the "real world" substantial utility of the present invention is further provided by the fact that there is an entire industry established based on the use of gene sequences or fragments thereof in a gene chip format. Perhaps the most notable gene chip company is Affymetrix. However, there are many companies which have, at one time or another, concentrated on the use of gene sequences or fragments, in gene chip and non-gene chip formats, for example: Gene Logic, ABI-Perkin-Elmer, HySeq and Incyte. In addition, one such company, Rosetta Inpharmatics, was viewed to have such "real world" value that it was acquired by large pharmaceutical company, Merck & Co., for substantial sums of money (net equity value of the transaction was $620 million). The "real world" substantial industrial utility of gene sequences or fragments would, therefore, appear to be widespread and well established. Clearly, persons of skill in the art, as well as venture capitalists and investors, readily recognize the utility, both scientific and commercial, of genomic data in general, and specifically human genomic data. Billions of dollars have been invested in the human genome project, resulting in useful genomic data (see, *e.g.*, Venter *et al.*, 2001, Science *291*:1304). The results have been a stunning success as the utility of human genomic data has been widely recognized as a great gift to humanity (see, *e.g.*, Jasny and Kennedy, 2001, Science *291*:1153). Clearly, the usefulness of human genomic data, such as the presently claimed nucleic acid molecules, is substantial and credible (worthy of billions of dollars and the creation of numerous companies focused on such information) and well-established (the utility of human genomic information has been clearly understood for many years). The sequences of

the present invention have particularly specific utility in DNA gene chip based analysis as they have been identified to contain several coding region nucleotide polymorphisms (see above), thus increasing their utility in DNA gene chip based analysis.

Finally, the Examiner is requested to consider the issue of due process. Applicants understanding is that issued United States patents retain a legal presumption of validity which in this case indicates that the inventions claimed in the cited patents are *legally presumed* to be in full compliance with the provisions of 35 U.S.C. sections 101, 102, 103, and 112. Applicants respectfully submit that, absent a change in the law as enacted by Congress and signed by the President, it is improper for the Examiner to hold Applicants' invention to a different legal standard of patentability. Given the rapid pace of development in the biotechnology arts, it is difficult for the Applicants to understand how an invention fully disclosed and free of prior art at the time the present application was filed, could somehow retain *less* utility and be *less* enabled than inventions in the cited issued U.S. patents (which were filed during a time when the level of skill in the art was clearly lower). Simply put, Applicants invention is *more* enabled and retains *at least as much* utility as the inventions described in the claims of the U.S. patents of record. Any argument to the contrary is at best arbitrary and at worst capricious. Absent authority provided by an act of Congress or Executive order, arbitrary or capricious conduct by an administrative office the U.S. government has historically proven to conflict with the provisions of the U.S. Constitution. The Patent Office does not have the authority to rewrite U.S. law. However, the Patent Office does have a Constitutional obligation to administer U.S. law in an unbiased and procedurally consistent manner. That is what the Applicants are respectfully requesting the Examiner to consider in the present matter. As the issued U.S. Patents cited above are presumed to meet <u>all</u> of the requirements for patentability, including 35 U.S.C. §§ 101 and 112, first paragraph, Applicants respectfully submit that the presently claimed polynucleotide must also meet the requirements of 35 U.S.C. § 101.

Thus in summary, Applicants submit that the presently claimed molecules have been shown to encode, as asserted in the specification as filed, ADAMSTS14 isoforms, whose biological function is known to the art. Thus, the present situation directly tracks Example 10 of the Revised Interim Utility Guidelines Training Materials (pages 53-55), which establishes that a rejection under 35 U.S.C. § 101 as allegedly lacking a patentable utility and under 35 U.S.C. § 112, first paragraph as allegedly unusable

by the skilled artisan due to the alleged lack of patentable utility, is not proper when a full length sequence (such as the presently claimed sequence), and has a similarity score greater than 95% to a protein having a known function. Furthermore this response has described a series of additional substantial, specific, credible and well-established utilities for the present invention. Therefore, Applicants submit that as the presently claimed sequence molecules have been shown to have a substantial, specific, credible and well-established utility, the rejection of the claims under 35 U.S.C. § 101 has been overcome. Thus, Applicants respectfully request that the rejection be withdrawn.

IV. Rejection of Claims 2-5 and 7-11 Under 35 U.S.C. § 112, First Paragraph

The Action next rejects claims 2-5 and 7-11 under 35 U.S.C. § 112, first paragraph, as allegedly the claimed invention is not supported by either a specific asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Applicants respectfully submit that claims 2-5 and 7-11 have been shown to have "a specific, substantial, and credible utility", as detailed in the section above. Therefore, one skilled in the art would clearly know how to use the claimed invention and Applicants therefore request that the rejection of claims. Therefore, Applicants submit that as the presently claimed sequence molecules have been shown to have a substantial, specific, credible and well-established utility, and thus the rejection of the claims under 35 U.S.C. § 112, first paragraph has been avoided. Thus, Applicants respectfully request that the rejection be withdrawn.

V. Rejection of Claim 7 Under 35 U.S.C. § 112, Second Paragraph

The Action next rejects claim 7 under 35 U.S.C. § 112, second paragraph, as being allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. While Applicants in no way agree, Claim 7 has been amended to replace the term "drawn" with the term 'selected".

Therefore, Applicants submit that amended Claim 7 is clearly definite and particularly points out and distinctly claims the subject matter which applicant regards as the invention and thus the rejection of the claim under 35 U.S.C. § 112, first paragraph has been avoided. Applicants, therefore,

respectfully request that the rejection be withdrawn.

VI. Conclusion

The present document is a full and complete response to the Action. In conclusion, Applicants submit that, in light of the foregoing remarks, the present case is in condition for allowance, and such favorable action is respectfully requested. Should Examiner Moore have any questions or comments, or believe that certain amendments of the claims might serve to improve their clarity, a telephone call to the undersigned Applicants' representative is earnestly solicited.

Respectfully submitted,

August 1, 2003
Date

Lance K. Ishimoto Reg. No. No. 41,866
Agent for Applicants

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24231
PATENT TRADEMARK OFFICE

Exhibit A

Status of Claims in

U.S. Patent Application Ser. No. 09/938,330

1.(cancelled)

2.(original) An isolated nucleic acid molecule comprising a nucleotide sequence that:

(a) encodes the amino acid sequence shown in SEQ ID NO: 20; and

(b) hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO: 19 or the complement thereof.

3.(original) An isolated nucleic acid molecule according to Claim 2 wherein said nucleotide sequence is present in cDNA.

4.(original) An isolated nucleic acid molecule encoding the amino acid sequence presented in SEQ ID NO:20.

5.(original) An isolated nucleic acid molecule encoding the amino acid sequence presented in SEQ ID NO:22.

6.(cancelled)

7.(currently amended) An isolated nucleic acid molecule comprising a nucleotide sequence encoding an amino acid sequence ~~drawn~~ <u>selected</u> from the group consisting of SEQ ID NOS: 20 and 22.

8.(previously presented) An expression vector comprising a nucleic acid sequence of Claim 4.

9.(previously presented) A cell comprising the expression vector of Claim 8.

10.(previously presented) An expression vector comprising a nucleic acid sequence of Claim 5.

11.(previously presented) A cell comprising the expression vector of Claim 10.

NCBI Entrez Protein

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Boo

Search Protein for Go Clear

Limits Preview/Index History Clipboard Details

Display FASTA Show: 20 Send to File Get Subsequence

☐ 1: Q8WXS8. ADAMTS-14 precurs...[gi:29337086] BLink, Domains, Links

```
LOCUS       Q8WXS8                  1223 aa            linear   PRI 15-SEP-2003
DEFINITION  ADAMTS-14 precursor (A disintegrin and metalloproteinase with
            thrombospondin motifs 14) (ADAM-TS 14) (ADAM-TS14).
ACCESSION   Q8WXS8
VERSION     Q8WXS8  GI:29337086
DBSOURCE    swissprot: locus AT14_HUMAN, accession Q8WXS8;
            class: standard.
            extra accessions:Q8TE55,Q8TEY8,created: Feb 28, 2003.
            sequence updated: Feb 28, 2003.
            annotation updated: Sep 15, 2003.
            xrefs: gi: 17483853, gi: 17483854, gi: 19171187, gi: 19171188, gi:
            18874445, gi: 18874446
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            607506, InterProIPR001762, InterProIPR001818, InterProIPR002870,
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            InterProIPR006025, PfamPF01562, PfamPF01421, PfamPF00090,
            PRINTSPR01705, SMARTSM00209, PROSITEPS50215, PROSITEPS00546,
            PROSITEPS00427, PROSITEPS50214, PROSITEPS50092, PROSITEPS00142
KEYWORDS    Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
            Collagen degradation; Repeat; Extracellular matrix; Alternative
            splicing; Alternative promoter usage.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 1223)
  AUTHORS   Bolz,H., Ramirez,A., von Brederlow,B. and Kubisch,C.
  TITLE     Characterization of ADAMTS14, a novel member of the ADAMTS
            metalloproteinase family
  JOURNAL   Biochim. Biophys. Acta 1522 (3), 221-225 (2001)
  MEDLINE   21638061
  REMARK    SEQUENCE FROM N.A. (ISOFORM A).
REFERENCE   2  (residues 1 to 1223)
  AUTHORS   Cal,S., Obaya,A.J., Llamazares,M., Garabaya,C., Quesada,V. and
            Lopez-Otin,C.
  TITLE     Cloning, expression analysis, and structural characterization of
            seven novel human ADAMTSs, a family of metalloproteinases with
            disintegrin and thrombospondin-1 domains
  JOURNAL   Gene 283 (1-2), 49-62 (2002)
  MEDLINE   21856482
  REMARK    SEQUENCE FROM N.A. (ISOFORM A).
            TISSUE=Fetal lung
REFERENCE   3  (residues 1 to 1223)
  AUTHORS   Colige,A., Vandenberghe,I., Thiry,M., Lambert,C.A., Van Beeumen,J.,
            Li,S.W., Prockop,D.J., Lapiere,C.M. and Nusgens,B.V.
  TITLE     Cloning and characterization of ADAMTS-14, a novel ADAMTS
            displaying high homology with ADAMTS-2 and ADAMTS-3
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  JOURNAL   J. Biol. Chem. 277 (8), 5756-5766 (2002)
  MEDLINE   21839041
  REMARK    SEQUENCE OF 29-1223 FROM N.A. (ISOFORMS B; C AND D), AND
            ALTERNATIVE PROMOTER USAGE.
COMMENT     -----------------------------------------------------------------
            This SWISS-PROT entry is copyright. It is produced through a
            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            -----------------------------------------------------------------.
            [FUNCTION] Has a aminoprocollagen type I activity processing
            activity in the absence of ADAMTS2. Seems to be synthesized as a
            latent enzyme that requires activation to display aminoprocollagen
            peptidase activity.
            [SUBCELLULAR LOCATION] Secreted. Associated with the extracellular
            matrix (By similarity).
            [ALTERNATIVE PRODUCTS] Event=Alternative promoter; Comment=2
            isoforms, A (shown here) and B, are produced by use of alternative
            promoters; Event=Alternative splicing; Named isoforms=4; Name=A;
            IsoId=Q8WXS8-1; Sequence=Displayed; Name=B; IsoId=Q8WXS8-2;
            Sequence=VSP_006958; Name=C; IsoId=Q8WXS8-3; Sequence=VSP_006958,
            VSP_005501; Note=Produced by alternative splicing of isoform B;
            Name=D; IsoId=Q8WXS8-4; Sequence=VSP_005501; Note=Produced by
            alternative splicing of isoform A.
            [TISSUE SPECIFICITY] Expressed in retina and at low levels in
            brain, lung and placenta. High expression in fetal tissues.
            [DOMAIN] The spacer domain and the TSP type-1 domains are important
            for a tight interaction with the extracellular matrix (By
            similarity).
            [PTM] The precursor is cleaved by a furin endopeptidase (By
            similarity).
            [SIMILARITY] Belongs to peptidase family M12B.
            [SIMILARITY] Contains 1 disintegrin-like domain.
            [SIMILARITY] Contains 1 PLAC domain.
            [SIMILARITY] Contains 4 TSP type-1 domains.
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                     /note="POTENTIAL."
     Region          23..252
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                     /note="G -> GMQG (in isoform C and isoform D).
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                     /note="CYS-RICH."
     Region          730..846
                     /gene="ADAMTS14"
                     /region_name="Domain"
                     /note="SPACER."
     Region          847..907
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     Region          868
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      121 lrpnrrlvvp gssvewqedf relfrqplrq ecvytggvtg mpgaavaisn cdglaglirt
      181 dstdffiepl ergqqekeas grthvvyrre avqqewaepd gdlhneafgl gdlpnllglv
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      781 mglewedave dakeslktsg plpeaiaila lppteggprs slaykyvihe dllpligsnn
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```
  901 cnqhpcsqpv wvteewgacs rscgklgvqt rgiqcllpls ngthkvmpak acagdrpear
  961 rpclrvpcpa qwrlgawsqc satcgegiqq rqvvcrtnan slghcegdrp dtvqvcslpa
 1021 cggnhqnstv radvwelgtp egqwvpqsep lhpinkisst epctgdrsvf cqmevldryc
 1081 sipgyhrlcc vscikkasgp npgpdpgpts lppfstpgsp lpgpqdpada aeppgkptgs
 1141 edhqhgratq lpgaldtssp gtqhpfapet pipgaswsis pttpgglpwg wtqtptpvpe
 1201 dkgqpgedlr hpgtslpaas pvt
//
```

```
 FASTA searches a protein or DNA sequence data bank
 version 3.3t05 March 30, 2000
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAARWaOhY: 1252 aa
 >Lex 221 SEQ ID NO:20
 vs  /tmp/fastaDAASWaOhY library
searching /tmp/fastaDAASWaOhY library

   1223 residues in     1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
 join: 40, opt: 28, gap-pen: -12/ -2, width:  16
 Scan time:  0.067
The best scores are:                                          opt
gi|29337086|sp|Q8WXS8|AT14_HUMAN ADAMTS-14 precur  (1223) 8686

>>gi|29337086|sp|Q8WXS8|AT14_HUMAN ADAMTS-14 precursor (  (1223 aa)
 initn: 8683 init1: 7506 opt: 8686
Smith-Waterman score: 8686;  98.611% identity in 1224 aa overlap (1-1224:1-1221)

               10        20        30        40        50        60
Lex     MAPLRALLSYLLPLHCALCXAAGSRTPELHLSGKLSDYGVTVPCSTDFRGRFLSHVVSGP
        ::::::::::::::::::: ::::::::::::::::::::::::::::::::::::::::
gi|293  MAPLRALLSYLLPLHCALCAAAGSRTPELHLSGKLSDYGVTVPCSTDFRGRFLSHVVSGP
               10        20        30        40        50        60

               70        80        90       100       110       120
Lex     AAASAGSMVVDTPPTLPRHSSHLRVARSPLHPGGTLWPGRVGRHSLYFNVTVFGKELHLR
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293  AAASAGSMVVDTPPTLPRHSSHLRVARSPLHPGGTLWPGRVGRHSLYFNVTVFGKELHLR
               70        80        90       100       110       120

              130       140       150       160       170       180
Lex     LRPNRRLVVPGSSVEWQEDFRELFRQPLRQECVYTGGVTGMPGAAVAISNCDGLAGLIRT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293  LRPNRRLVVPGSSVEWQEDFRELFRQPLRQECVYTGGVTGMPGAAVAISNCDGLAGLIRT
              130       140       150       160       170       180

              190       200       210       220       230       240
Lex     DSTDFFIEPLERGQQEKEASGRTHVVYRREAVQQEWAEPDGDLHNEAFGLGDLPNLLGLV
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293  DSTDFFIEPLERGQQEKEASGRTHVVYRREAVQQEWAEPDGDLHNEAFGLGDLPNLLGLV
              190       200       210       220       230       240

              250       260       270       280       290       300
Lex     GDQLGDTERKRRHAKPGSYSIEVLLVVDDSVVRFHGKEHVQNYVLTLMNIVDEIYHDESL
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293  GDQLGDTERKRRHAKPGSYSIEVLLVVDDSVVRFHGKEHVQNYVLTLMNIVDEIYHDESL
              250       260       270       280       290       300

              310       320       330       340       350       360
Lex     GVHINIALVRLIMVGYRQSLSLIERGNPSRSLEQVCRWAHSQQRQDPSHAEHHDHVVFLT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293  GVHINIALVRLIMVGYRQSLSLIERGNPSRSLEQVCRWAHSQQRQDPSHAEHHDHVVFLT
              310       320       330       340       350       360

              370       380       390       400       410       420
Lex     RQDFGPSGYAPVTGMCHPLRSCALNHEDGFSSAFVIAHETGHVLGMEHDGQGNGCADETS
```

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              ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293        RQDFGPSGYAPVTGMCHPLRSCALNHEDGFSSAFVIAHETGHVLGMEHDGQGNGCADETS
                      370       380       390       400       410       420

                      430       440       450       460       470       480
Lex           LGSVMAPLVQAAFHRFHWSRCSKLELSRYLPSYDCLLDDPFDPAWPQPPELPGINYSMDE
              ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293        LGSVMAPLVQAAFHRFHWSRCSKLELSRYLPSYDCLLDDPFDPAWPQPPELPGINYSMDE
                      430       440       450       460       470       480

                      490       500       510       520       530       540
Lex           QCRFDFGSGYQTCLAFRTFEPCKQLWCSHPDNXXFCKTKKGPPLDGTECAPGKWCFKGHC
              ::::::::::::::::::::::::::::::::  ::::::::::::::::::::::::::
gi|293        QCRFDFGSGYQTCLAFRTFEPCKQLWCSHPDNPYFCKTKKGPPLDGTECAPGKWCFKGHC
                      490       500       510       520       530       540

                      550       560       570       580       590       600
Lex           IWKSPEQTYGQDGGWSSWTKFGSCSRSCGGGVRSRSRSCNNPSPAYGGRXCLGPMFEYQV
              ::::::::::::::::::::::::::::::::::::::::::::::::: ::::::::::
gi|293        IWKSPEQTYGQDGGWSSWTKFGSCSRSCGGGVRSRSRSCNNPSPAYGGRPCLGPMFEYQV
                      550       560       570       580       590       600

                      610       620       630       640       650       660
Lex           CNSEECPGTYEDFRAQQCAKRNXYYVHQNAKHXWVPYEPDDDAQKCELICQSADXGDVVF
              :::::::::::::::::::::: ::::::::: ::::::::::::::::::::: :::::
gi|293        CNSEECPGTYEDFRAQQCAKRNSYYVHQNAKHSWVPYEPDDDAQKCELICQSADTGDVVF
                      610       620       630       640       650       660

                      670       680       690       700       710       720
Lex           MNQVVHDGTRCSYRDPYSVCARGECVPVGCDKEVGSMKADDKCGVCGGDNSHCRTVKGTL
              ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293        MNQVVHDGTRCSYRDPYSVCARGECVPVGCDKEVGSMKADDKCGVCGGDNSHCRTVKGTL
                      670       680       690       700       710       720

                      730       740       750       760       770       780
Lex           GKASKQAGALKLVQIPAGARHIQIEALEKSPHXXVVKNQVTGSFILNPKGKEATSRTFTA
              ::::::::::::::::::::::::::::::::  ::::::::::::::::::::::::::
gi|293        GKASKQAGALKLVQIPAGARHIQIEALEKSPHRIVVKNQVTGSFILNPKGKEATSRTFTA
                      730       740       750       760       770       780

                      790       800       810       820       830       840
Lex           MGLEWEDAVEDAKESLKTSGPLPEAIAILALPPTEGGPRSSLAYKYVIHEDLLPLIGSNN
              ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293        MGLEWEDAVEDAKESLKTSGPLPEAIAILALPPTEGGPRSSLAYKYVIHEDLLPLIGSNN
                      790       800       810       820       830       840

                      850       860       870       880       890       900
Lex           VLLEEMDTYEWALKSWAPCSKACGGGIQFTKYGCRRRRDHHMVQRHLCDHKKRPKPIRRR
              ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293        VLLEEMDTYEWALKSWAPCSKACGGGIQFTKYGCRRRRDHHMVQRHLCDHKKRPKPIRRR
                      850       860       870       880       890       900

                      910       920       930       940       950       960
Lex           CNQHPCSQPVWVTEEWGACSRSCGKLGVQTRGIQCLLPLSNGTHKVMPAKACAGDRPEAR
              ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293        CNQHPCSQPVWVTEEWGACSRSCGKLGVQTRGIQCLLPLSNGTHKVMPAKACAGDRPEAR
                      910       920       930       940       950       960

                      970       980       990      1000      1010      1020
Lex           RPCLRVPCPAQWRLGAWSQCSATCGEGIQQRQVVCRTNANSLGHCEGDRPDTVQVCXLPA
```

```
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::: :::
gi|293    RPCLRVPCPAQWRLGAWSQCSATCGEGIQQRQVVCRTNANSLGHCEGDRPDTVQVCSLPA
                   970       980       990      1000      1010      1020

                  1030      1040      1050      1060      1070      1080
Lex       CGGNHQNSTVRADVWELGTPEGQWVPQSXPLHPINKISSMCAAEPCTGDRSVFCQMEVLD
          :::::::::::::::::::::::::::: ::::::::::   .:::::::::::::::::
gi|293    CGGNHQNSTVRADVWELGTPEGQWVPQSEPLHPINKISS---TEPCTGDRSVFCQMEVLD
                  1030      1040      1050         1060      1070

                  1090      1100      1110      1120      1130      1140
Lex       RYCSIPGYHRLCCVSCIKKASGPNPGPDPGPTSLPPFSTPGSPLPGPQDPADAAEPPGKP
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293    RYCSIPGYHRLCCVSCIKKASGPNPGPDPGPTSLPPFSTPGSPLPGPQDPADAAEPPGKP
        1080      1090      1100      1110      1120      1130

                  1150      1160      1170      1180      1190      1200
Lex       TGSEDHQHGRATQLPGALDTSSPGTQHPFAPETPIPGASWSISPTTPGGLPWGWTQTPTP
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|293    TGSEDHQHGRATQLPGALDTSSPGTQHPFAPETPIPGASWSISPTTPGGLPWGWTQTPTP
        1140      1150      1160      1170      1180      1190

                  1210      1220      1230      1240      1250
Lex       VPEDKGQPGEDLRHPGTSLPADLPGRPPEPCHPTGTFTLCVLPRDSQLRGHT
          :::::::::::::::::::::   :
gi|293    VPEDKGQPGEDLRHPGTSLPAASPVT
        1200      1210      1220
```

```
1252 residues in 1 query   sequences
1223 residues in 1 library sequences
 Scomplib [version 3.3t05 March 30, 2000]
 start: Tue Jul 29 17:17:39 2003 done: Tue Jul 29 17:17:40 2003
 Scan time:  0.067 Display time:  2.117

Function used was FASTA
```

EXHIBIT “D”

J Biol Chem. 2002 Feb 22;277(8):5756-66. Epub 2001 Dec 07. Related Articles, Links

Full text article at www.jbc.org

Cloning and characterization of ADAMTS-14, a novel ADAMTS displaying high homology with ADAMTS-2 and ADAMTS-3.

Colige A, Vandenberghe I, Thiry M, Lambert CA, Van Beeumen J, Li SW, Prockop DJ, Lapiere CM, Nusgens BV.

Laboratory of Connective Tissues Biology, Experimental Cancerology Research Center, Tour de Pathologie (B23/3), University of Liege, B-4000 Liege, Belgium.

The processing of amino- and carboxyl-propeptides of fibrillar collagens is required to generate collagen monomers that correctly assemble into fibrils. Mutations in the ADAMTS2 gene, the aminopropeptidase of procollagen I and II, result in the accumulation of non-fully processed type I procollagen, causing human Ehlers-Danlos syndrome type VIIC and animal dermatosparaxis. In this study, we show that the aminopropeptide of type I procollagen can be cleaved in vivo in absence of ADAMTS-2 activity and that this processing is performed at the cleavage site for ADAMTS-2. In an attempt to identify the enzyme responsible for this alternative aminoprocollagen peptidase activity, we have cloned the cDNA and determined the primary structure of human and mouse ADAMTS-14, a novel ADAMTS displaying striking homologies with ADAMTS-2 and -3. The structure of the human gene, which maps to 10q21.3, and the mechanisms of generation of the various transcripts are described. The existence of two sites of initiation of transcription, in two different promoter contexts, suggests that transcripts resulting from these two sites can be differently regulated. The tissue distribution of ADAMTS-14, the regulation of the gene expression by various cytokines and the activity of the recombinant enzyme are evaluated. The potential function of ADAMTS-14 as a physiological aminoprocollagen peptidase in vivo is discussed.

PMID: 11741898 [PubMed - indexed for MEDLINE]

Gene. 2002 Jan 23;283(1-2):49-62. Related Articles, Links
ELSEVIER SCIENCE
FULL-TEXT ARTICLE

Cloning, expression analysis, and structural characterization of seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains.

Cal S, Obaya AJ, Llamazares M, Garabaya C, Quesada V, Lopez-Otin C.

Departamento de Bioquimica y Biologia Molecular, Facultad de Medicina, Instituto Universitario de Oncologia, Universidad de Oviedo, 33006, Oviedo, Spain.

ADAMTS (A Disintegrin And Metalloproteinase domain, with ThromboSpondin type-1 modules) is a recently described family of zinc-dependent proteases which play important roles in a variety of normal and pathological conditions, including arthritis and cancer. In this work, we report the identification and cloning of cDNAs encoding seven new human ADAMTSs. These novel enzymes have been called ADAMTS-13, -14, -15, -16, -17, -18, and -19. All of them show a domain organization similar to that of previously characterized family members, consisting of a signal sequence, a propeptide, a metalloproteinase domain, a disintegrin-like domain, a cysteine-rich region, and a variable number of TS-1 repeats. Expression analysis revealed that these ADAMTS genes are mainly expressed in fetal tissues, especially in lung (ADAMTS14, ADAMTS16, ADAMTS17, ADAMTS18, and ADAMTS19), kidney (ADAMTS14, ADAMTS15, and ADAMTS16), and liver (ADAMTS13, ADAMTS15 and ADAMTS18). Reverse transcriptase--polymerase chain reaction analysis also revealed the expression of some of these new ADAMTSs in different human adult tissues, such as prostate (ADAMTS13, ADAMTS17, and ADAMTS18), and brain (ADAMTS13, ADAMTS16, ADAMTS17, and ADAMTS18). High levels of ADAMTSs transcripts were also observed in some tumor biopsies and cells lines, including osteosarcomas (ADAMTS19), melanoma and colon carcinoma cells (ADAMTS13). Chromosomal location analysis indicated that the seven identified ADAMTS genes are dispersed in the human genome mapping to 9q34, 10q21, 11q25, 5p15, 15q24, 16q23, and 5q31, respectively. According to these results, together with a comparative analysis of ADAMTSs in other eukaryotic organisms, we conclude that these enzymes, with at least 18 distinct members encoded within the human genome, represent an example of a widely expanded protease family during metazoan evolution.

PMID: 11867212 [PubMed - indexed for MEDLINE]

Biochim Biophys Acta. 2001 Dec 30;1522(3):221-5. Related Articles, Links
ELSEVIER SCIENCE
FULL-TEXT ARTICLE

Characterization of ADAMTS14, a novel member of the ADAMTS metalloproteinase family.

Bolz H, Ramirez A, von Brederlow B, Kubisch C.

Institut fur Hmangentik, Universitats-Klinikum Eppendorf, Hamburg, Germany. bolz@uke.uni-hamburg.de

ADAMTS (a disintegrin-like and metalloproteinase domain with thrombospondin type 1 modules) proteins constitute a family of zinc metalloproteinases which target and process extracellular matrix proteins. We cloned and characterized a novel human ADAMTS gene, ADAMTS14, which is located on human chromosome 10q2. ADAMTS14 exhibits the characteristic multidomain structure of ADAMTS proteins including four thrombospondin modules and shows highest similarity to ADAMTS3 and ADAMTS2. By RT-PCR analysis we demonstrated that ADAMTS14 is expressed in human retina and also at low levels in adult brain, lung and placenta.

PMID: 11779638 [PubMed - indexed for MEDLINE]

EXHIBIT "E"

MegaBlast

```
MEGABLAST 1.2.3-Paracel [2001-11-20]
Reference:
Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.
Database: Homo_sapiens.latestgp.masked.fa
           33,840 sequences; 200,810,911,373 total letters

Query= LEX221seqid19
         (3759 letters)
                                                                 Score     E
Sequences producing significant alignments:                      (bits)  Value

AL355344.20.1.149490                                               882   0.0
AC007484.2.50228.57677                                             854   0.0
AC069538.10.1.169772                                               654   0.0
AC007484.2.23991.29266                                             654   0.0
AC007484.2.57778.65289                                             387   e-104
AC007484.2.112555.124636                                           314   3e-82
AC010216.8.1.110753                                                139   1e-29

>AL355344.20.1.149490
          Length = 149490

 Score =  882 bits (444), Expect = 0.0
 Identities = 444/444 (100%)
 Strand = Plus / Plus


Query: 80     cagagctgcacctctctggaaagctcagtgactatggtgtgacagtgccctgcagcacag 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 147159 cagagctgcacctctctggaaagctcagtgactatggtgtgacagtgccctgcagcacag 147218


Query: 140    actttcggggacgcttcctctcccacgtggtgtctggcccagcagcagcctctgcaggga 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 147219 actttcggggacgcttcctctcccacgtggtgtctggcccagcagcagcctctgcaggga 147278


Query: 200    gcatggtagtggacacgccacccacactaccacgacactccagtcacctccgggtggctc 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 147279 gcatggtagtggacacgccacccacactaccacgacactccagtcacctccgggtggctc 147338


Query: 260    gcagccctctgcacccaggagggaccctgtggcctggcagggtggggcgccactccctct 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 147339 gcagccctctgcacccaggagggaccctgtggcctggcagggtggggcgccactccctct 147398


Query: 320    acttcaatgtcactgttttcgggaaggaactgcacttgcgcctgcggcccaatcggaggt 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 147399 acttcaatgtcactgttttcgggaaggaactgcacttgcgcctgcggcccaatcggaggt 147458


Query: 380    tggtagtgccaggatcctcagtggagtggcaggaggattttcgggagctgttccggcagc 439
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 147459 tggtagtgccaggatcctcagtggagtggcaggaggattttcgggagctgttccggcagc 147518

Query: 440    ccttacggcaggagtgtgtgtacactggaggtgtcactggaatgcctggggcagctgttg 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 147519 ccttacggcaggagtgtgtgtacactggaggtgtcactggaatgcctggggcagctgttg 147578

Query: 500    ccatcagcaactgtgacggattgg 523
              ||||||||||||||||||||||||
Sbjct: 147579 ccatcagcaactgtgacggattgg 147602


 Score =  159 bits (80), Expect = 1e-35
 Identities = 81/82 (98%)
 Strand = Plus / Plus

Query: 1      atggctccactccgcgcgctgctgtcctacctgctgcctttgcactgtgcgctctgcrcc 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct: 145409 atggctccactccgcgcgctgctgtcctacctgctgcctttgcactgtgcgctctgcgcc 145468

Query: 61     gccgcgggcagccggaccccag 82
              ||||||||||||||||||||||
Sbjct: 145469 gccgcgggcagccggaccccag 145490


>AC007484.2.50228.57677
          Length = 7450

 Score =  854 bits (430), Expect = 0.0
 Identities = 441/444 (99%), Gaps = 3/444 (0%)
 Strand = Plus / Minus

Query: 80   cagagctgcacctctctggaaagctcagtgactatggtgtgacagtgccctgcagcacag 139
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5458 cagagctgcacctctctggaaagctcagtgactatggtgtgacagtgccctgcagcacag 5399

Query: 140  actttcggggacgcttcctctcccacgtggtgtctggcccagcagcagcctctgcaggga 199
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5398 actttcggggacgcttcctctcccacgtggtgtctggcccagcagcagcctctgcaggga 5339

Query: 200  gcatggtagtggacacgccacccacactaccacgacactccagtcacctccgggtggctc 259
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5338 gcatggtagtggacacgccacccacactaccacgacactccagtcacctccgggtggctc 5279

Query: 260  gcagccctctgcacccaggagggaccctgtggcctggcagggtggggcgccactccctct 319
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query: 320   acttcaatgtcactgttttcgggaaggaactgcacttgcgcctgcggcccaatcggaggt 379
             |||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
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Query: 380   tggtagtgccaggatcctcagtggagtggcaggaggattttcgggagctgttccggcagc 439
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5160  tggtagtgccaggatcctcagtggagtggcaggaggattttcgggagctgttccggcag- 5102

Query: 440   ccttacggcaggagtgtgtgtacactggaggtgtcactggaatgcctggggcagctgttg 499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5101  ccttacggcaggagtgtgtgtacactggaggtgtcactggaatgcctggggcagctgttg 5042

Query: 500   ccatcagcaactgtgacggattgg 523
             ||||||||||||||||||||||||
Sbjct: 5041  ccatcagcaactgtgacggattgg 5018
```

```
 Score =  133 bits (67), Expect = 7e-28
 Identities = 79/83 (95%), Gaps = 3/83 (3%)
 Strand = Plus / Minus
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```
Query: 1     atggctccactccgcgcgctgctgtcctacctgctgcctttgc-actgtgcgctctgcrc 59
             ||||||||||||||||||||||||||||||||||||||||||| ||||| |||||||| |
Sbjct: 7207  atggctccactccgcgcgctgctgtcctacctgctgcctttgcaactgt-cgctctgcgc 7149

Query: 60    cgccgcgggcagccggaccccag 82
             | |||||||||||||||||||||
Sbjct: 7148  c-ccgcgggcagccggaccccag 7127
```

```
>AC069538.10.1.169772
          Length = 169772

 Score =  654 bits (329), Expect = 0.0
 Identities = 336/338 (99%), Gaps = 1/338 (0%)
 Strand = Plus / Minus
```

```
Query: 3337    tcactgccccccttctccactcctggaagccccttaccaggaccccaggaccctgcagat 3396
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132825  tcactgccccccttctccactcctggaagccccttaccaggaccccaggaccctgcagat 132766

Query: 3397    gctgcagagcctcctggaaagccaacgggatcagaggaccatcagcatggccgagccaca 3456
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132765  gctgcagagcctcctggaaagccaacgggatcagaggaccatcagcatggccgagccaca 132706
```

```
Query: 3457   cagctcccaggagctctggatacaagctccccagggacccagcatccctttgcccctgag 3516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132705 cagctcccaggagctctggatacaagctccccagggacccagcatccctttgcccctgag 132646

Query: 3517   acaccaatccctggagcatcctggagcatctcccctaccacccccgggggctgccttgg 3576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132645 acaccaatccctggagcatcctggagcatctcccctaccacccccgggggctgccttgg 132586

Query: 3577   ggctggactcagacacctacgccagtccctgaggacaaagggcaacctggagaagacctg 3636
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132585 ggctggactcagacacctacgccagtccctgaggacaaagggcaacctggagaagacctg 132526

Query: 3637   agacatcccggcaccagcctccctgctgacctgcccgg 3674
              |||||||||||||||||||||||||||| ||| |||||
Sbjct: 132525 agacatcccggcaccagcctccctgctg-cctccccgg 132489
```

Score = 405 bits (204), Expect = e-110
Identities = 207/208 (99%)
Strand = Plus / Minus

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Query: 2730   gtgggtgacggaggagtggggtgcctgcagccggagctgtgggaagctgggggtgcagac 2789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 139531 gtgggtgacggaggagtggggtgcctgcagccggagctgtgggaagctgggggtgcagac 139472

Query: 2790   acgggggatacagtgcctgctgcccctctccaatggaacccacaaggtcatgccggccaa 2849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 139471 acgggggatacagtgcctgctgcccctctccaatggaacccacaaggtcatgccggccaa 139412

Query: 2850   agcctgcgccggggaccggcctgaggcccgacggccctgtctccgagtgccctgcccagc 2909
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 139411 agcctgtgccggggaccggcctgaggcccgacggccctgtctccgagtgccctgcccagc 139352

Query: 2910   ccagtggaggctgggagcctggtcccag 2937
              ||||||||||||||||||||||||||||
Sbjct: 139351 ccagtggaggctgggagcctggtcccag 139324
```

Score = 340 bits (171), Expect = 5e-90
Identities = 171/171 (100%)
Strand = Plus / Minus

```
Query: 2427   ggctctccccccaactgagggtggcccccgcagcagcctggcctacaagtacgtcatcca 2486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 141854 ggctctccccccaactgagggtggcccccgcagcagcctggcctacaagtacgtcatcca 141795
```

```
Query: 2487   tgaggacctgctgccccttatcgggagcaacaatgtgctcctggaggagatggacaccta 2546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 141794 tgaggacctgctgccccttatcgggagcaacaatgtgctcctggaggagatggacaccta 141735

Query: 2547   tgagtgggcgctcaagagctgggccccctgcagcaaggcctgtggaggagg 2597
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 141734 tgagtgggcgctcaagagctgggccccctgcagcaaggcctgtggaggagg 141684
```

```
 Score =  338 bits (170), Expect = 2e-89
 Identities = 173/176 (98%)
 Strand = Plus / Minus
```

```
Query: 1749   cccagcctatggaggccgccygtgcttagggcccatgttcgagtaccaggtctgcaacag 1808
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct: 152344 cccagcctatggaggccgcctgtgcttagggcccatgttcgagtaccaggtctgcaacag 152285

Query: 1809   cgaggagtgccctgggacctacgaggacttccgggcccagcagtgtgccaagcgcaactc 1868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 152284 cgaggagtgccctgggacctacgaggacttccgggcccagcagtgtgccaagcgcaactc 152225

Query: 1869   stactatgtgcaccagaatgccaagcacagstgggtgccctacgagcctgacgatg 1924
               ||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct: 152224 ctactatgtgcaccagaatgccaagcacagctgggtgccctacgagcctgacgatg 152169
```

```
 Score =  330 bits (166), Expect = 4e-87
 Identities = 166/166 (100%)
 Strand = Plus / Minus
```

```
Query: 2263   gtggtgaagaaccaggtcaccggcagcttcatcctcaaccccaagggcaaggaagccaca 2322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143510 gtggtgaagaaccaggtcaccggcagcttcatcctcaaccccaagggcaaggaagccaca 143451

Query: 2323   agccggaccttcaccgccatgggcctggagtgggaggatgcggtggaggatgccaaggaa 2382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143450 agccggaccttcaccgccatgggcctggagtgggaggatgcggtggaggatgccaaggaa 143391

Query: 2383   agcctcaagaccagcgggcccctgcctgaagccattgccatcctgg 2428
              ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143390 agcctcaagaccagcgggcccctgcctgaagccattgccatcctgg 143345
```

```
 Score =  306 bits (154), Expect = 7e-80
 Identities = 158/159 (99%), Gaps = 1/159 (0%)
 Strand = Plus / Minus
```

```
Query: 952    cagtccctgagcctgatcgagcgcgggaacccctcacgcagcctggagcaggtgtgtcgc 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 163232 cagtccctgagcctgatcgagcgcgggaacccctcacgcagcctggagcaggtgtgtcgc 163173

Query: 1012   tgggcacactcccagcagcgccaggaccccagccacgctgagcaccatgaccacgttgtg 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 163172 tgggcacactcccagcagcgccaggaccccagccacgctgagcaccatgaccacgttgtg 163113

Query: 1072   ttcctcacccggcaggactttgggccctcagggtatgca 1110
              |||||||||||||||||||||||||||||||| ||||||
Sbjct: 163112 ttcctcacccggcaggactttgggccctcagg-tatgca 163075


 Score =  300 bits (151), Expect = 4e-78
 Identities = 151/151 (100%)
 Strand = Plus / Minus


Query: 1598   agtggtgcttcaaaggtcactgcatctggaagtcgccggagcagacatatggccaggatg 1657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 154491 agtggtgcttcaaaggtcactgcatctggaagtcgccggagcagacatatggccaggatg 154432

Query: 1658   gaggctggagctcctggaccaagtttgggtcatgttcgcggtcatgtgggggcggggtgc 1717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 154431 gaggctggagctcctggaccaagtttgggtcatgttcgcggtcatgtgggggcggggtgc 154372

Query: 1718   gatcccgcagccggagctgcaacaacccctc 1748
              |||||||||||||||||||||||||||||||
Sbjct: 154371 gatcccgcagccggagctgcaacaacccctc 154341


 Score =  286 bits (144), Expect = 6e-74
 Identities = 144/144 (100%)
 Strand = Plus / Minus


Query: 1209   gctcggcatggagcatgacggtcaggggaatggctgtgcagatgagaccagcctgggcag 1268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 159446 gctcggcatggagcatgacggtcaggggaatggctgtgcagatgagaccagcctgggcag 159387

Query: 1269   cgtcatggcgcccctggtgcaggctgccttccaccgcttccattggtcccgctgcagcaa 1328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 159386 cgtcatggcgcccctggtgcaggctgccttccaccgcttccattggtcccgctgcagcaa 159327

Query: 1329   gctggagctcagccgctacctccc 1352
              ||||||||||||||||||||||||
Sbjct: 159326 gctggagctcagccgctacctccc 159303
```

```
 Score =  274 bits (138), Expect = 2e-70
 Identities = 138/138 (100%)
 Strand = Plus / Minus

Query: 2595   agggatccagttcaccaaatacggctgccggcgcagacgagaccaccacatggtgcagcg 2654
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 141238 agggatccagttcaccaaatacggctgccggcgcagacgagaccaccacatggtgcagcg 141179

Query: 2655   acacctgtgtgaccacaagaagaggcccaagcccatccgccggcgctgcaaccagcaccc 2714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 141178 acacctgtgtgaccacaagaagaggcccaagcccatccgccggcgctgcaaccagcaccc 141119

Query: 2715   gtgctctcagcctgtgtg 2732
              ||||||||||||||||||
Sbjct: 141118 gtgctctcagcctgtgtg 141101


 Score =  264 bits (133), Expect = 2e-67
 Identities = 134/135 (99%)
 Strand = Plus / Minus

Query: 1924   gacgcccagaagtgtgagctgatctgccagtcggcggacacrggggacgtggtgttcatg 1983
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct: 149784 gacgcccagaagtgtgagctgatctgccagtcggcggacacgggggacgtggtgttcatg 149725

Query: 1984   aaccaggtggttcacgatgggacacgctgcagctaccgggacccatacagcgtctgtgcg 2043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 149724 aaccaggtggttcacgatgggacacgctgcagctaccgggacccatacagcgtctgtgcg 149665

Query: 2044   cgtggcgagtgtgtg 2058
              |||||||||||||||
Sbjct: 149664 cgtggcgagtgtgtg 149650


 Score =  264 bits (133), Expect = 2e-67
 Identities = 133/133 (100%)
 Strand = Plus / Minus

Query: 1353   ctcctacgactgcctcctcgatgacccctttgatcctgcctggccccagcccccagagct 1412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 158162 ctcctacgactgcctcctcgatgacccctttgatcctgcctggccccagcccccagagct 158103

Query: 1413   gcctgggatcaactactcaatggatgagcagtgccgctttgactttggcagtggctacca 1472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 158102 gcctgggatcaactactcaatggatgagcagtgccgctttgactttggcagtggctacca 158043
```

```
Query: 1473   gacctgcttggca 1485
              |||||||||||||
Sbjct: 158042 gacctgcttggca 158030


 Score =  262 bits (132), Expect = 1e-66
 Identities = 133/134 (99%)
 Strand = Plus / Minus


Query: 2935   cagtgctctgccacctgtggagagggcatccagcagcggcaggtggtgtgcaggaccaac 2994
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 135372 cagtgctctgccacctgtggagagggcatccagcagcggcaggtggtgtgcaggaccaac 135313


Query: 2995   gccaacagcctcgggcattgcgagggggataggccagacactgtccaggtctgcarcctg 3054
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct: 135312 gccaacagcctcgggcattgcgagggggataggccagacactgtccaggtctgcagcctg 135253


Query: 3055   cccgcctgtggagg 3068
              ||||||||||||||
Sbjct: 135252 cccgcctgtggagg 135239


 Score =  254 bits (128), Expect = 2e-64
 Identities = 128/128 (100%)
 Strand = Plus / Minus


Query: 3179   tgtgtgcagcggagccctgcacgggagacaggtctgtcttctgccagatggaagtgctcg 3238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132983 tgtgtgcagcggagccctgcacgggagacaggtctgtcttctgccagatggaagtgctcg 132924


Query: 3239   atcgctactgctccattcccggctaccaccggctctgctgtgtgtcctgcatcaagaagg 3298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132923 atcgctactgctccattcccggctaccaccggctctgctgtgtgtcctgcatcaagaagg 132864


Query: 3299   cctcgggc 3306
              ||||||||
Sbjct: 132863 cctcgggc 132856


 Score =  250 bits (126), Expect = 4e-63
 Identities = 126/126 (100%)
 Strand = Plus / Minus


Query: 2058   gcctgtcggctgtgacaaggaggtggggtccatgaaggcggatgacaagtgtggagtctg 2117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 149266 gcctgtcggctgtgacaaggaggtggggtccatgaaggcggatgacaagtgtggagtctg 149207

Query: 2118   cgggggtgacaactcccactgcaggactgtgaaggggacgctgggcaaggcctccaagca 2177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 149206 cgggggtgacaactcccactgcaggactgtgaaggggacgctgggcaaggcctccaagca 149147

Query: 2178   ggcagg 2183
              ||||||
Sbjct: 149146 ggcagg 149141


 Score =  221 bits (111), Expect = 4e-54
 Identities = 112/113 (99%)
 Strand = Plus / Minus

Query: 3066   aggaaatcaccagaactccacggtgagggccgatgtctgggaacttgggacgccagaggg 3125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 135158 aggaaatcaccagaactccacggtgagggccgatgtctgggaacttgggacgccagaggg 135099

Query: 3126   gcagtgggtgccacaatctgraccccctacatcccattaacaagatatcatcaa 3178
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct: 135098 gcagtgggtgccacaatctgaaccccctacatcccattaacaagatatcatcaa 135046


 Score =  219 bits (110), Expect = 1e-53
 Identities = 112/114 (98%)
 Strand = Plus / Minus

Query: 1486   ttcaggacctttgagccctgcaagcagctgtggtgcagccatcctgacaaccmgtayttc 1545
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||
Sbjct: 156651 ttcaggacctttgagccctgcaagcagctgtggtgcagccatcctgacaacccgtacttc 156592

Query: 1546   tgcaagaccaagaaggggcccccgctggatgggactgagtgtgcacccggcaag 1599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 156591 tgcaagaccaagaaggggcccccgctggatgggactgagtgtgcacccggcaag 156538


 Score =  219 bits (110), Expect = 1e-53
 Identities = 110/110 (100%)
 Strand = Plus / Minus

Query: 1100   cagggtatgcacccgtcactggcatgtgtcacccccctgaggagctgtgccctcaaccatg 1159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 161080 cagggtatgcacccgtcactggcatgtgtcacccccctgaggagctgtgccctcaaccatg 161021

Query: 1160   aggatggcttctcctcagccttcgtgatagctcatgagaccggccacgtg 1209
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 161020 aggatggcttctcctcagccttcgtgatagctcatgagaccggccacgtg 160971


 Score =  167 bits (84), Expect = 5e-38
 Identities = 84/84 (100%)
 Strand = Plus / Minus


Query: 871    gtagatgagatttaccacgatgagtccctggggggttcatataaatattgccctcgtccgc 930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 164037 gtagatgagatttaccacgatgagtccctggggggttcatataaatattgccctcgtccgc 163978


Query: 931    ttgatcatggttggctaccgacag 954
              ||||||||||||||||||||||||
Sbjct: 163977 ttgatcatggttggctaccgacag 163954


 Score =  161 bits (81), Expect = 3e-36
 Identities = 81/81 (100%)
 Strand = Plus / Minus


Query: 2178   ggcaggagctctcaagctggtgcagatcccagcaggtgccaggcacatccagattgaggc 2237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 148110 ggcaggagctctcaagctggtgcagatcccagcaggtgccaggcacatccagattgaggc 148051


Query: 2238   actggagaagtccccccaccg 2258
              |||||||||||||||||||||
Sbjct: 148050 actggagaagtccccccaccg 148030


 Score =  145 bits (73), Expect = 2e-31
 Identities = 73/73 (100%)
 Strand = Plus / Minus


Query: 3687   gccctgccatcccactggcacgtttacactctgtgtactgccccgtgactcccagctcag 3746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 132475 gccctgccatcccactggcacgtttacactctgtgtactgccccgtgactcccagctcag 132416


Query: 3747   aggacacacatag 3759
              |||||||||||||
Sbjct: 132415 aggacacacatag 132403


 Score = 89.9 bits (45), Expect = 1e-14
 Identities = 66/73 (90%)
 Strand = Plus / Minus
```

```
Query: 1375   gacccctttgatcctgcctggccccagcccccagagctgcctgggatcaactactcaatg 1434
              ||||||||||| ||  ||||||||||||||||||||||||| |||||| ||| |||||||
Sbjct: 158909 gacccctttgagcccacctggccccagcccccagagctgcccgggatcgacttctcaatg 158850

Query: 1435   gatgagcagtgcc 1447
              ||||| |||||||
Sbjct: 158849 gatgaacagtgcc 158837


>AC007484.2.23991.29266
          Length = 5276

 Score =  654 bits (329), Expect = 0.0
 Identities = 336/338 (99%), Gaps = 1/338 (0%)
 Strand = Plus / Minus


Query: 3337 tcactgccccccttctccactcctggaagccccttaccaggaccccaggaccctgcagat 3396
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2310 tcactgccccccttctccactcctggaagccccttaccaggaccccaggaccctgcagat 2251

Query: 3397 gctgcagagcctcctggaaagccaacgggatcagaggaccatcagcatggccgagccaca 3456
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2250 gctgcagagcctcctggaaagccaacgggatcagaggaccatcagcatggccgagccaca 2191

Query: 3457 cagctcccaggagctctggatacaagctccccagggacccagcatccctttgcccctgag 3516
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2190 cagctcccaggagctctggatacaagctccccagggacccagcatccctttgcccctgag 2131

Query: 3517 acaccaatccctggagcatcctggagcatctcccctaccaccccgggggctgccttgg 3576
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2130 acaccaatccctggagcatcctggagcatctcccctaccaccccgggggctgccttgg 2071

Query: 3577 ggctggactcagacacctacgccagtccctgaggacaaagggcaacctggagaagacctg 3636
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2070 ggctggactcagacacctacgccagtccctgaggacaaagggcaacctggagaagacctg 2011

Query: 3637 agacatcccggcaccagcctccctgctgacctgcccgg 3674
            ||||||||||||||||||||||||||||  ||| |||||
Sbjct: 2010 agacatcccggcaccagcctccctgctg-cctccccgg 1974


 Score =  262 bits (132), Expect = 1e-66
 Identities = 133/134 (99%)
 Strand = Plus / Minus


Query: 2935 cagtgctctgccacctgtggagagggcatccagcagcggcaggtggtgtgcaggaccaac 2994
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4860 cagtgctctgccacctgtggagagggcatccagcagcggcaggtggtgtgcaggaccaac 4801

Query: 2995 gccaacagcctcgggcattgcgaggggatagccagacactgtccaggtctgcarcctg 3054
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct: 4800 gccaacagcctcgggcattgcgaggggatagccagacactgtccaggtctgcagcctg 4741

Query: 3055 cccgcctgtggagg 3068
            ||||||||||||||
Sbjct: 4740 cccgcctgtggagg 4727


 Score =  254 bits (128), Expect = 2e-64
 Identities = 128/128 (100%)
 Strand = Plus / Minus

Query: 3179 tgtgtgcagcggagccctgcacgggagacaggtctgtcttctgccagatggaagtgctcg 3238
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2468 tgtgtgcagcggagccctgcacgggagacaggtctgtcttctgccagatggaagtgctcg 2409

Query: 3239 atcgctactgctccattcccggctaccaccggctctgctgtgtgtcctgcatcaagaagg 3298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2408 atcgctactgctccattcccggctaccaccggctctgctgtgtgtcctgcatcaagaagg 2349

Query: 3299 cctcgggc 3306
            ||||||||
Sbjct: 2348 cctcgggc 2341


 Score =  221 bits (111), Expect = 4e-54
 Identities = 112/113 (99%)
 Strand = Plus / Minus

Query: 3066 aggaaatcaccagaactccacggtgagggccgatgtctgggaacttgggacgccagaggg 3125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4646 aggaaatcaccagaactccacggtgagggccgatgtctgggaacttgggacgccagaggg 4587

Query: 3126 gcagtgggtgccacaatctgraccccctacatcccattaacaagatatcatcaa 3178
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct: 4586 gcagtgggtgccacaatctgaacccctacatcccattaacaagatatcatcaa 4534


 Score =  145 bits (73), Expect = 2e-31
 Identities = 73/73 (100%)
 Strand = Plus / Minus
```

```
Query: 3687 gccctgccatcccactggcacgtttacactctgtgtactgccccgtgactcccagctcag 3746
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1960 gccctgccatcccactggcacgtttacactctgtgtactgccccgtgactcccagctcag 1901


Query: 3747 aggacacacatag 3759
            |||||||||||||
Sbjct: 1900 aggacacacatag 1888


>AC007484.2.57778.65289
          Length = 7512

 Score =  387 bits (195), Expect = e-104
 Identities = 195/195 (100%)
 Strand = Plus / Minus


Query: 678   agcctttggcctgggagaccttcccaacctgctgggcctggtgggggaccagctgggcga 737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2978 agcctttggcctgggagaccttcccaacctgctgggcctggtgggggaccagctgggcga 2919


Query: 738   cacagagcggaagcggcggcatgccaagccaggcagctacagcatcgaggtgctgctggt 797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2918 cacagagcggaagcggcggcatgccaagccaggcagctacagcatcgaggtgctgctggt 2859


Query: 798   ggtggacgactcggtggttcgcttccatggcaaggagcatgtgcagaactatgtcctcac 857
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2858 ggtggacgactcggtggttcgcttccatggcaaggagcatgtgcagaactatgtcctcac 2799


Query: 858   cctcatgaatatcgt 872
             |||||||||||||||
Sbjct: 2798 cctcatgaatatcgt 2784


>AC007484.2.112555.124636
          Length = 12082

 Score =  314 bits (158), Expect = 3e-82
 Identities = 158/158 (100%)
 Strand = Plus / Plus


Query: 522    ggcgggcctcatccgcacagacagcaccgacttcttcattgagcctctggagcggggcca 581
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10474 ggcgggcctcatccgcacagacagcaccgacttcttcattgagcctctggagcggggcca 10533


Query: 582    gcaggagaaggaggccagcgggaggacacatgtggtgtaccgccgggaggccgtccagca 641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 10534 gcaggagaaggaggccagcgggaggacacatgtggtgtaccgccgggaggccgtccagca 10593
```

```
Query: 642   ggagtgggcagaacctgacggggacctgcacaatgaag 679
             ||||||||||||||||||||||||||||||||||||||
Sbjct: 10594 ggagtgggcagaacctgacggggacctgcacaatgaag 10631


>AC010216.8.1.110753
          Length = 110753

 Score =  139 bits (70), Expect = 1e-29
 Identities = 101/112 (90%), Gaps = 4/112 (3%)
 Strand = Plus / Plus


Query: 1490  ggacctttgagccctgcaagcagctgtggtgcagccatcctgacaaccmgtayttctgca 1549
             |||||||||| |||||||||||||||||||||||||||||||||||||   || || ||||
Sbjct: 32976 ggacctttgacccctgcaagcagctgtggtgcagccatcctgacaacccctacttttgca 33035


Query: 1550  agaccaagaaggggcccccgct-ggatgggactga-gtgtgcacccggcaag 1599
             ||||||||||||||||||| || ||| |||||| | ||||||||| ||||||
Sbjct: 33036 agaccaagaaggggccccc-cttggacgggact-atgtgtgcacctggcaag 33085


 Score =  129 bits (65), Expect = 1e-26
 Identities = 83/89 (93%)
 Strand = Plus / Plus


Query: 1261  ctgggcagcgtcatggcgcccctggtgcaggctgccttccaccgcttccattggtcccgc 1320
             ||||||||| |||||||||||||||||||||| ||||||||||||||||| |||||||||
Sbjct: 31087 ctgggcagcatcatggcgcccctggtgcaggccgccttccaccgcttccactggtcccgc 31146


Query: 1321  tgcagcaagctggagctcagccgctacct 1349
             |||||| ||| |||||| |||||||||||
Sbjct: 31147 tgcagccagcaggagctgagccgctacct 31175
```